Docket #: S25-493

Three-Dimensional Tumor Bed Reconstruction to Predict Recurrence Risk After Neoadjuvant Chemotherapy

Stanford researchers have developed a method for reconstructing a resected tumor bed in three dimensions and deriving quantitative measurements of how residual tumor is distributed, which predict cancer recurrence after neoadjuvant chemotherapy. The method uses digital specimen X-ray or brightfield images already captured during routine surgical pathology and requires no additional tissue, imaging, or laboratory steps.

Pathologists currently report post-chemotherapy response as simply the presence or absence of residual tumor, and any residual disease triggers escalated adjuvant treatment. This binary readout leads to widespread over- and under-treatment. This technology recovers each tissue block's original position within the breast and overlays its disease status to quantify the spatial spread of residual tumor. Patients who later relapsed showed a dispersed, moth-eaten pattern of chemoresistant deposits, whereas cured patients showed compact, focused disease. Disease status can be scored by routine histopathology (either read out by a pathologist or computer-assisted), or by genomic sequencing, including Stanford's related spatial minimal residual disease (sMRD) assay (Stanford Docket S23-414), with which this reconstruction method can be paired for a combined molecular and spatial risk assessment.

Stage of Development
Pre-Clinical

Applications

- Recurrence risk assessment after neoadjuvant chemotherapy to guide adjuvant treatment decisions
- Risk stratification in other solid tumors treated with neoadjuvant chemotherapy, such as bladder and rectal cancers and sarcomas
- Surgical pathology software for tumor bed reconstruction and spatial risk reporting
- Patient selection and stratification for adjuvant clinical trials

Advantages

- First three-dimensional tumor bed reconstruction used to assign relapse risk
- Uses images and tissue blocks already generated in routine pathology workflows
- Distinguishes risk among patients that current pathologic scoring groups together
- Works without genomic sequencing, but is compatible with it
- Histopathology readout may be human (pathologist) or computer-assisted
- Applicable to any serially sectioned resection specimen

Publications

- Ransohoff, J. D., Carleton, M. A., Miron Barroso, S., et al. (2025). Abstract P4-03-17: Enhanced spatial detection of post-neoadjuvant breast cancer minimal residual disease by tissue-based Cancer Personalized Profiling by Deep Sequencing. Clinical Cancer Research, 31(12_Supplement), P4-03-17.
- Ransohoff, J. D., Carleton, M. A., Miron Barroso, S., et al. (2025).Abstract 6352: Defining spatial molecular residual disease by personalized tumor tissue profiling. Cancer Research, 85(8_Supplement_1), 6352.

Patents

- Published Application: STAN-2319PRV

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